

▼ MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50
◆ ▼ YEWLDPISKTEWSREEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100
▼ EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150
MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200
▼ KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKLRQQLDGE 250
▼ ◆ LRSEKEGRDRKKDKQHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300
▼ QISDAELQEVVKGQASEIARQTAEESGITNSASSTLLSEYNVTNNVAL 350
◆ ● RTPRTPASQDRILQEAQNLMALTNVDTPLKGGLNTPLHESDFSGVTPORO 400
▼ VVQTPNTVLSTPFRTPSNGAEGLTPRSGTTPKPVINSTPGRTPLRDKLNI 450
NPEDGMADYSDPSYVKOMERRESREHLRLGLLGLPAPKNDFEIVLPENAEK 500
▼ ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550
VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPGNKKG 600
▼ KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGMSHG 650
▼ ◆ ELSSEAYNQVWEECYSQVL^YLPQSQRYTRANLASKDRIESLEKRLEINR 700
GHMTTEAKRAAKMEKKMKILLGGYQSRAGLMKQLNDLWDQIEQAHLELR 750
▼ TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLK 800

KF*

Fig. 1A

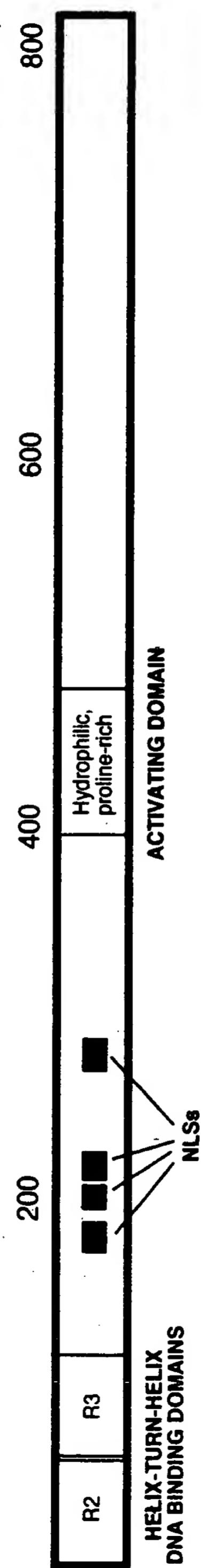


Fig. 1B

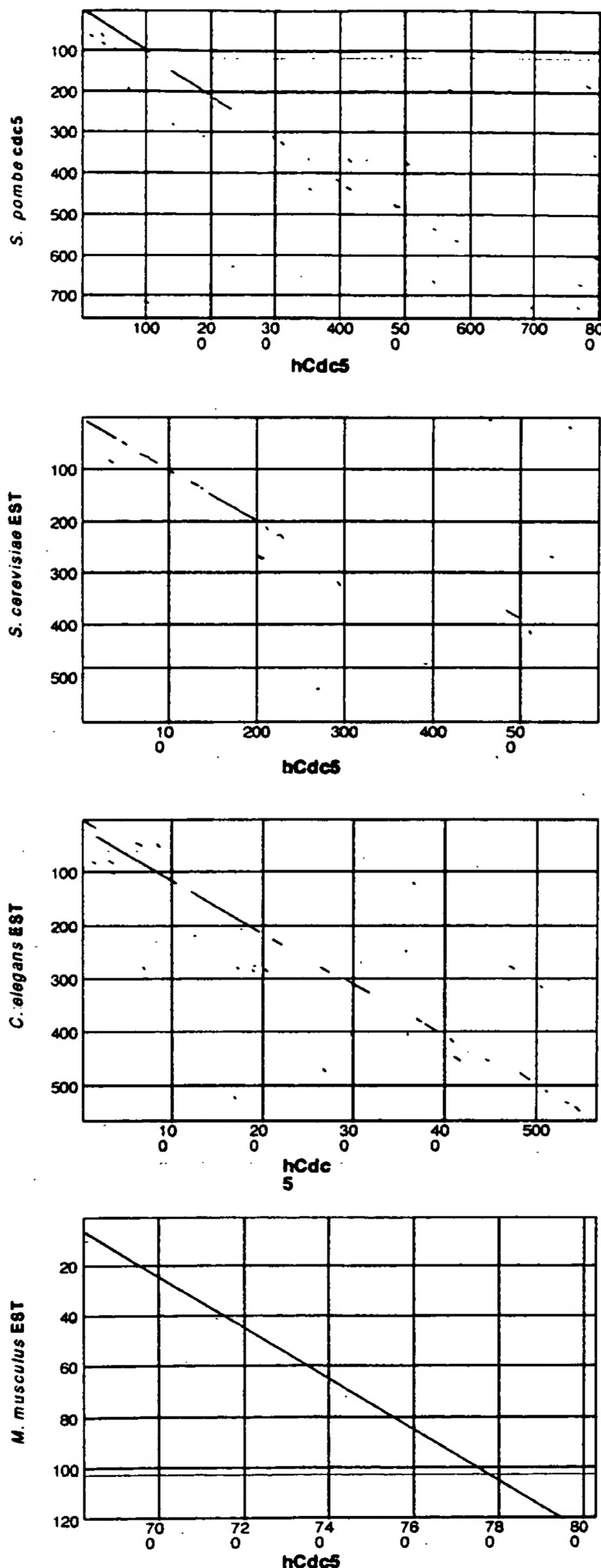


Fig. 2A



IKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARWYEWLDP (6-56)
LKGGAWKNTEDEILKAAVSKYGKNQWARISSLVRKITPKQCKARWYEWIDP (5-55)
VK-GPWTKEEDQKVIELVKKYGTQWTTLIAKHLKGRLGKQCERWHNHLP (88-137)
IK-GPWTKEEDQRVIELVQKYGPKRWSLIAKHLKGRIIGKQCERWHNHLP (87-136)
IK-GPWTKEEDQRVIELVQKYGPKRWSVIAKHLKGRIIGKQCERWHNHLP (92-141)

HCdc5
Spambead5
bMyb
aMyb
cMyb

Fig. 2B



hCdc5	PLKGGLNTPLHESDFSGVTPQRQVVQTPNNTVLSTPFRTPSNGAEGLTPRSGTTPKVINSTP (378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGV - PSHAANGS --- ALAAP --- Q -- A T P (380-434)
b-Myb	PVK - TL - PFSPSQFLNFWNKQDTLESPSLTSTPVCSQKVVTTPPLHRDKTPLHQKHAAF (445-503)
a-Myb	IIRKKRKMRVGHSPGSEL - RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)

hCdc5	GRTPLRDKLNINPDEGMADYSDPDSYVKQMERESREHLRLGLLGLPAPKNDFEIVLPENAEK (440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAEEAERAGR-LASE-REN-KIRLKALRELLAKLPKPKNDYEL-ME-P-R- (435-487)
b-Myb	VTPDQKYSMNDNTPHTP-TPFKNAKYGPLKPHLEEDLKEVLSEAGIELIIIEDDIRP (504-565)
a-Myb	TSTPICGGQKAL-ITTPLHKETTPKDKENVGFRTPTTIRRSILGTPRTPTPFKNALAAQEKK (509-569)

Fig. 2C

APR 22 2004

5' untranslated region:

GGCACGAGGAGGAAGTGGCGCTTGAGTCGGTOGCCAATCGCTGTTACTACTTCCTGAGCTCCCTCGGCTGCTTGC
CGAGACACCCCTGCCGCCAAG

Coding region:

1 DNA BINDING DOMAIN ()

1 acgccccqaa tcatgatcaa qqqqqqqcqra cqqaqqqaaa ccggaggatqa aattctcgaaa
61 qcaqccqtaa tqaaataatqq qaaaaaattcaq cqatccatqqa ttatccatcatt qctgcataqa
121 aaarcacqcaaa agcaatqcaa acccaqaaqqq ractgaatqqa cqgatccaad catcaagaag
181 acacaatqqr ccqaaqaaga adaggaaaaa ctcctqcact cqgccaactt qatqccaact
241 caqccqaaqa ccattqccccc aatcatqqa aqaacacqaa cccaaqccccc aqaacacat
301 qaattttttc tqqataaaqdc tgcccaaaaga gacaatgaag aggaaaacaac agatgatcca
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat
421 ccaattgata tggatgagga tgaacttgag atgcttctg aagccagagc ccgcctggct

2 NUCLEAR LOCALIZATION DOMAIN ()

481 aatactcagg gaaagaaggc caagaggaaa qcaagagaga aacaattgga agaagcaaga
541 cgtcttgctq ccctccaaaa aagaagagaa cttcgagcaq ctggcataga aattcaqaag
601 aaaagaaaaa ggaagagagg agttgattat aatgccgaaa tcccatttga aaaaaaqcct
661 gcccttggct ttatgatac ttctgagggaa aactaccaag ctcttgacgc agatttcagg
721 aaattaqac aacaggatct tgatggggag ctaagatctq aaaaagaagg aqagataga
781 aaaaaagaca aacagcatc qaaaaggaaa aaagaatctg atttaccatc agctattctt
841 caaactagtg gtgttctga atttactaaa aagagaagca aactagtact tcctgcccct
901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaaagcgag tgaaattgca
961 cgtcaaactg ccgaggaatc tggcataaca aattctgctt ccagtacact tttgtctgag
1021 tacaatgtca ccaacaacag cgttgcttt agaacaccac gaacaccagc ttcccaggac
1081 agaattctgc aggaagccca gaacctcatg gcccacca atgtggacac cccattgaaa

3 ACTIVATION DOMAIN ()

1141 ggtggactta ataccccatt qcatqagagt qacttctcaq qtqtaactcc acaqcgacaa
1201 qttqtaqaqta ctccaaacac agttctctt actccattca qqactccttc taatggagct
1261 qaaqqqctqa ctccccqqaq tqqaacaact cccaaaccaq ttatatactc tactccqqqt
1321 aqaactcctc ttccqagacaa qttaaacatt aatcccqagg atqqaatqgc aqactataqt
1381 gatccctctt acgtqaaqca qatqqaaga qaatcccqag aacatctccg tttagggttg
1441 ttgggccttc ctgcccctaa gaatgattt gaaattgttc taccagaaaa tgccgagaag
1501 gagctggaaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct
1561 cggaaagcagg ccatacgaga tgcagagcgt gtaaaaggaaa taaaacgaaat gcaaaagct
1621 gtccagaaag atctgccaag accatcagaa gtaaaatgaaa ctatctaag acccttaaat
1681 gtagAACCGC cttaacaga ttacagaaa agtgaagaac taatcaaaaa agaaatgatc
1741 acaatgcttc attatgaccc tctacatcac ctttatgaac catctggaaa taaaaaggc
1801 aaaactgttag ggttttgtac caataattca gagcacatta cctatctgga acataatcct
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttgt gcaggagatg
1921 gaagtggta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccaggcg
1981 tgggaagaat gctacagtca agttttatat cttcctggc agagccgcta cacacgggccc
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcg gataaacagg
2101 ggtcacatga cgacagaagc caagagggt gcaaagatgg aaaagaagat gaaaattttg
2161 cttgggggtt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatggac
2221 caaattgaac aggtcactt ggagttacgc acttttgaa aactcaagaa acatgaagat
2281 tctgctattc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaaagagac tttaaagtca
2401 aaattctgt

untranslated region:

AGTACAGTTATTCCTGTACAGGATTAATTAAATTGCCGTTTCACTCTAGAAGGCTGAACTG ATGTTTATCTTCATTGACA
AATTTACCCACCATTGTGGTTTTCACTTGTATTTAAATGATATCGATCTTACACATTCTGTATAAAGACCTTAACTCCACA
GGACGGACATTTAGACTTTAAATTATTA AGCTATCATTCTTTAGTAAATGTCATATTGCAAACTTTTAGTTTGGCCTTTAA
TTTAAAAAGCTAATTAAAGTGTGCTGCCGTGAGTAACTCTTGAATAAAAACAAAATATAAAA

Fig. 2D

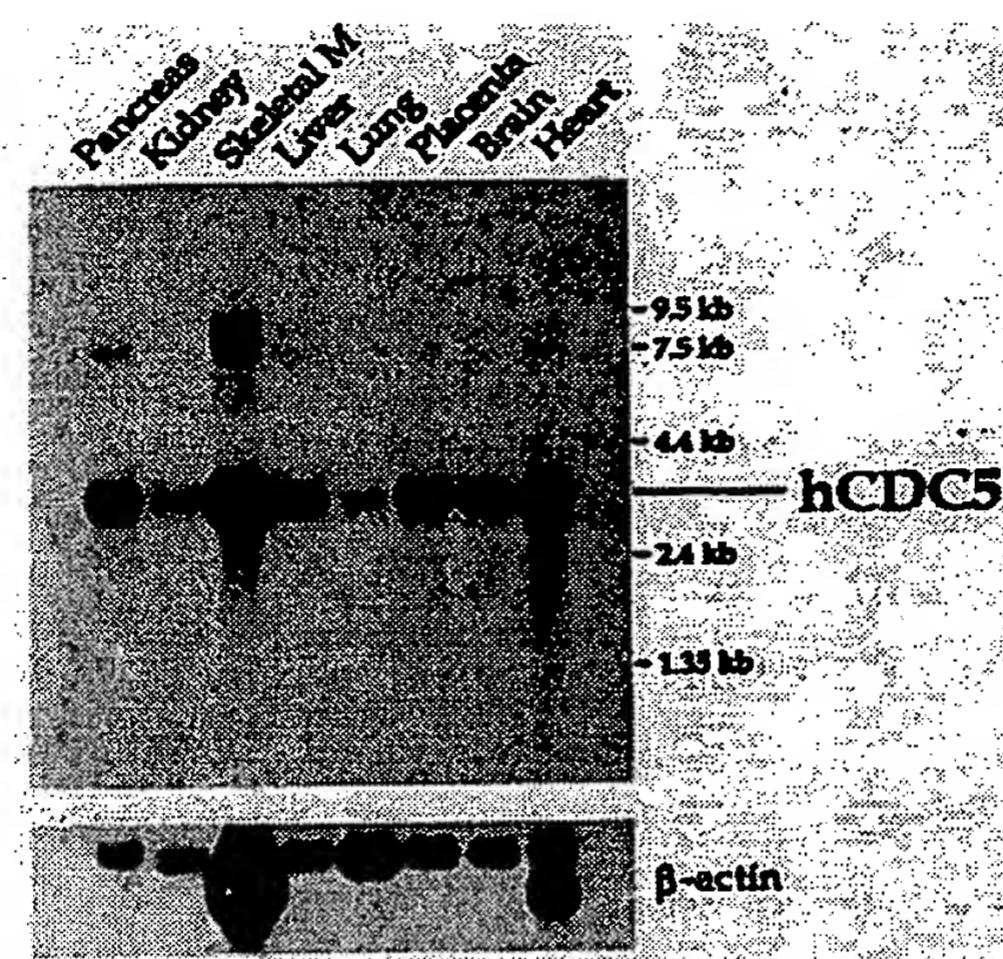


FIG. 3

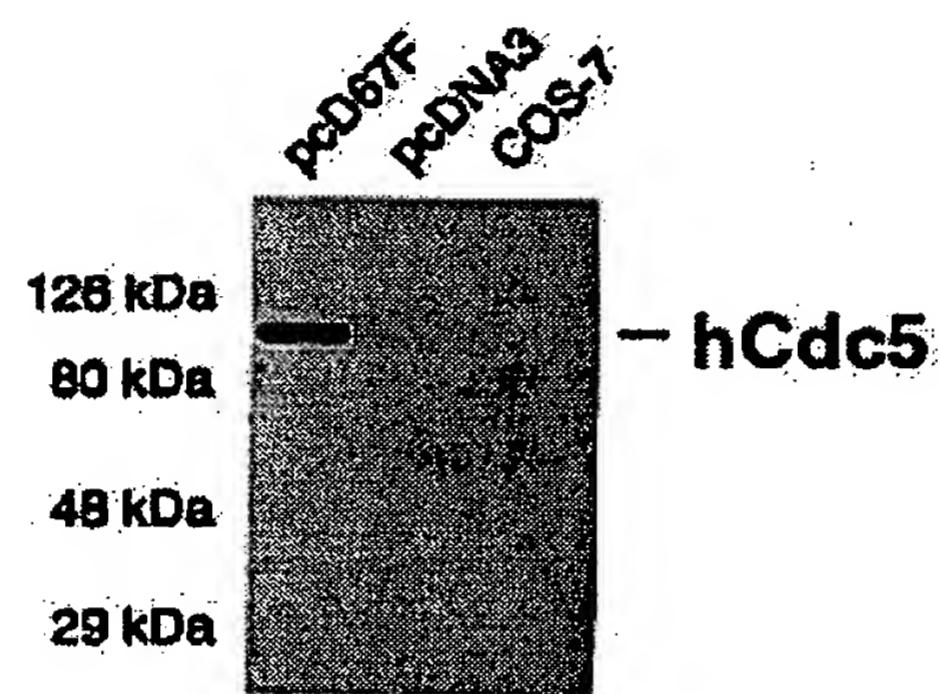
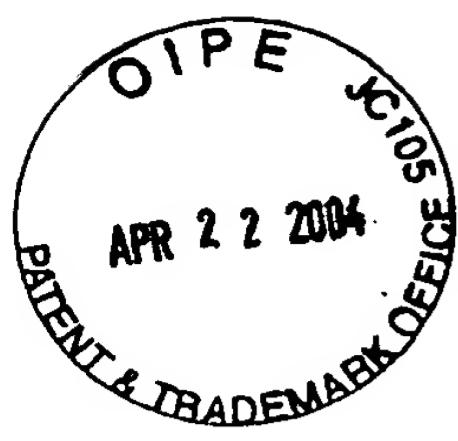


FIG. 4A

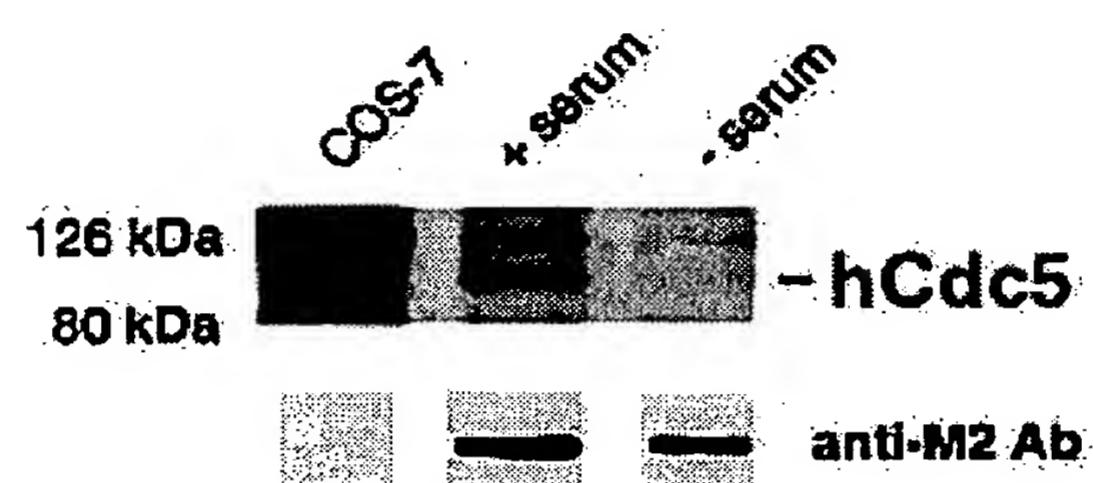


FIG. 4B

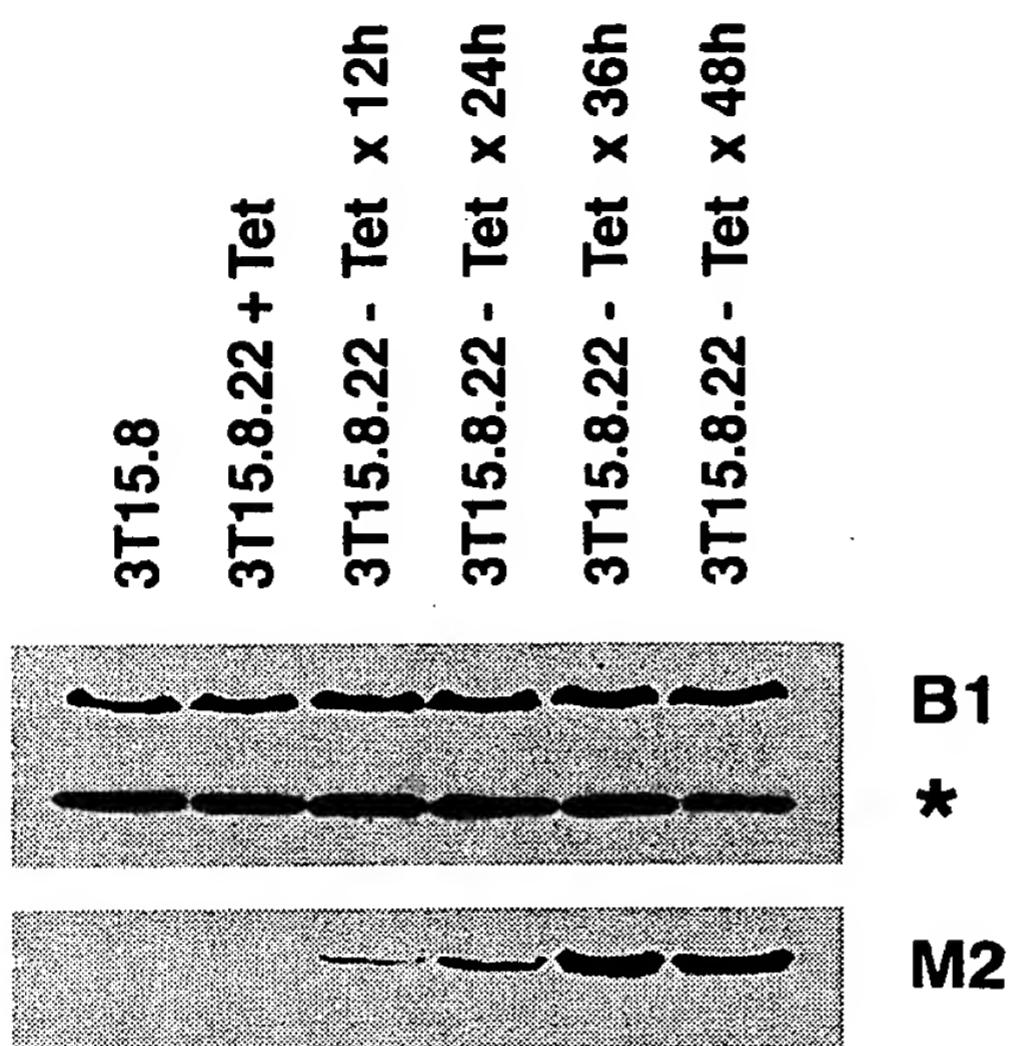


FIG. 5

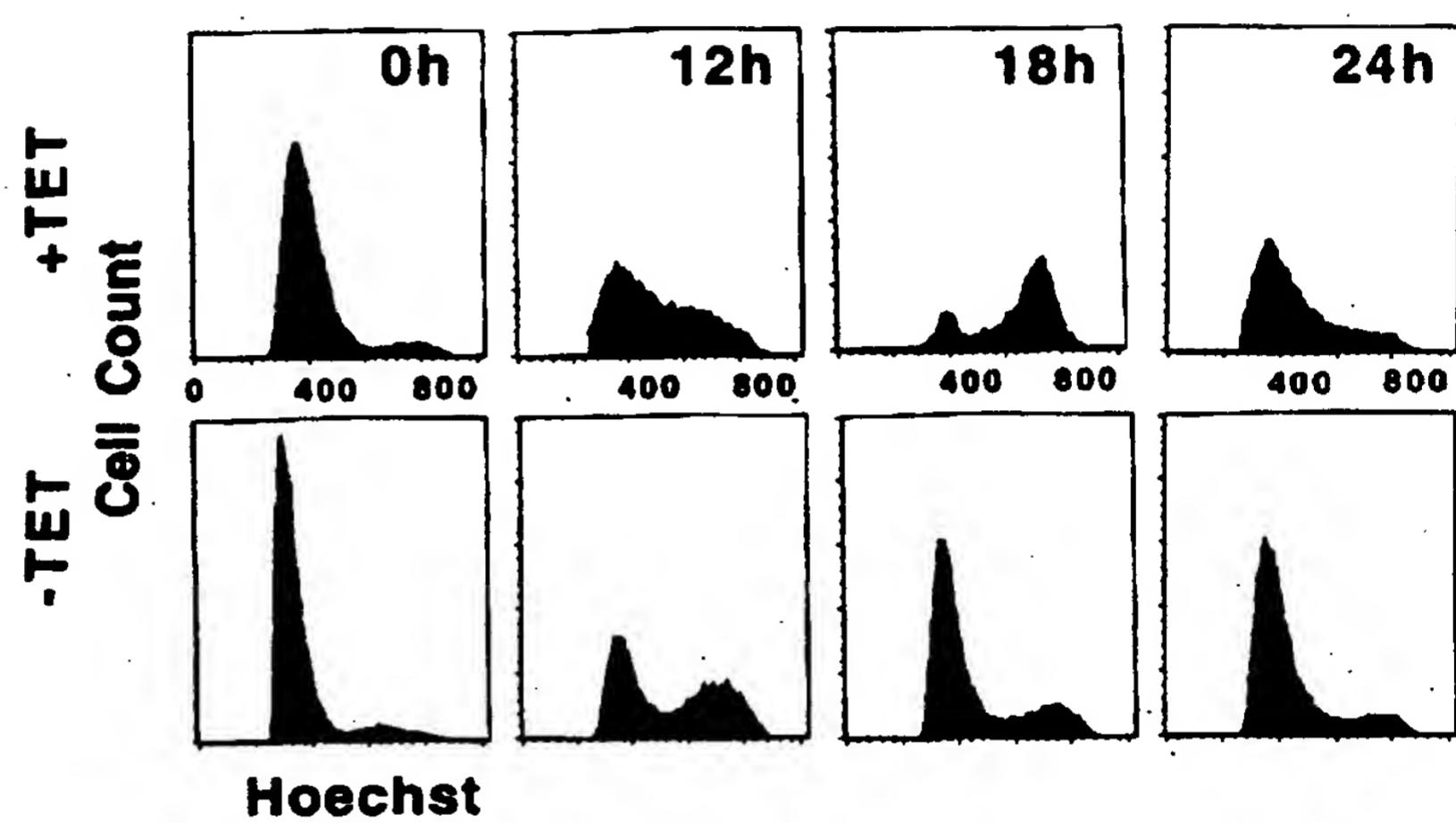


Fig. 6

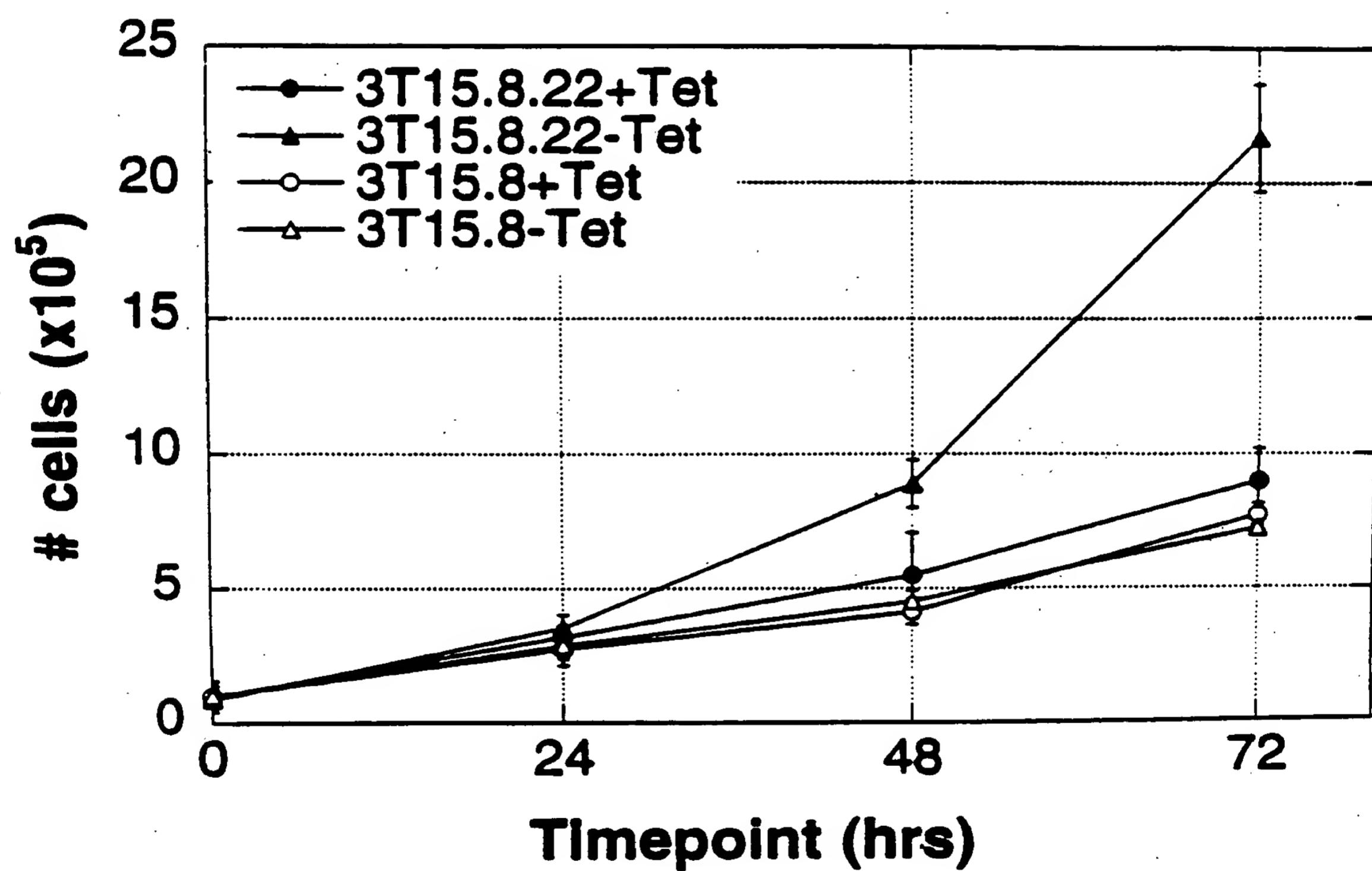


Fig. 7

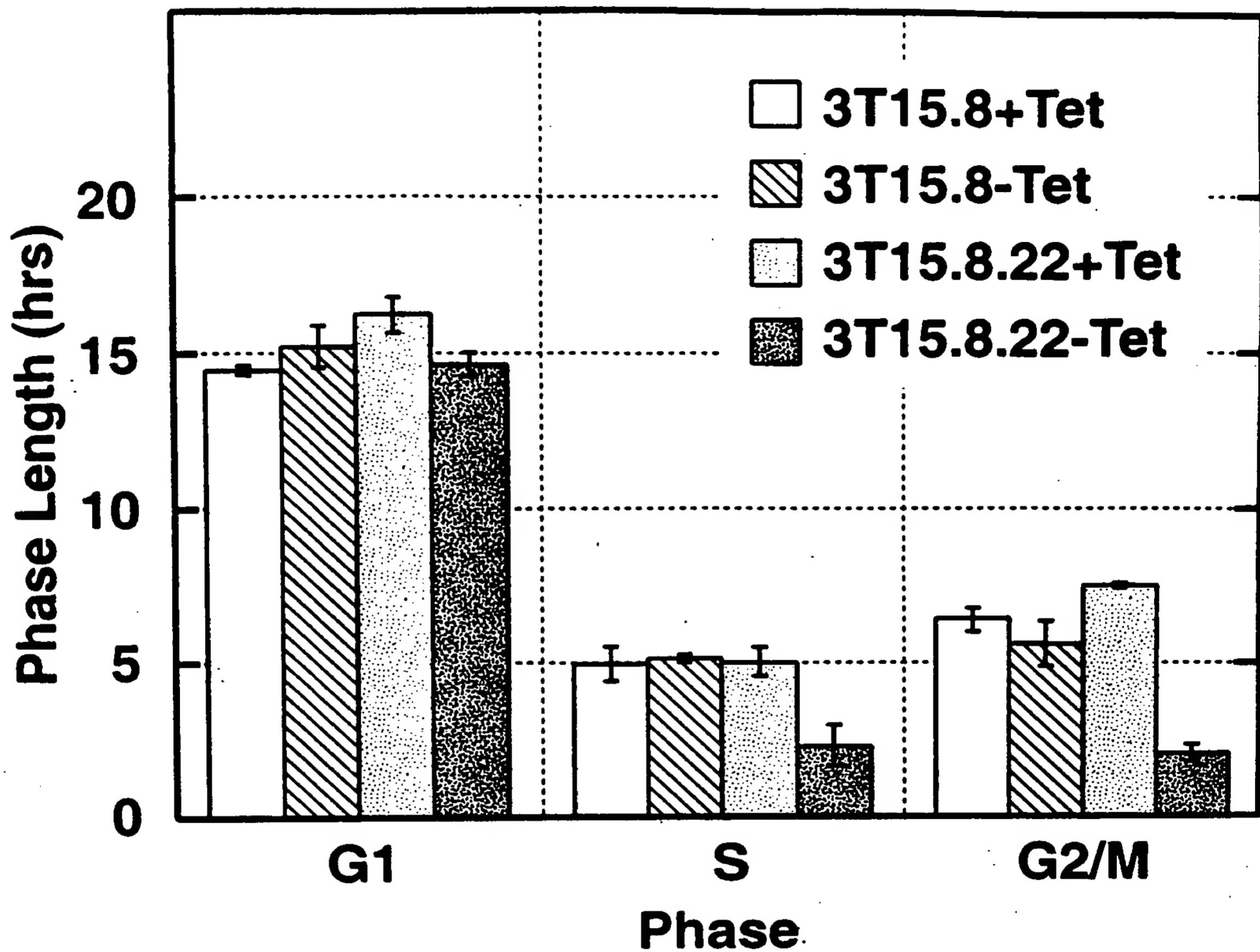


FIG. 8

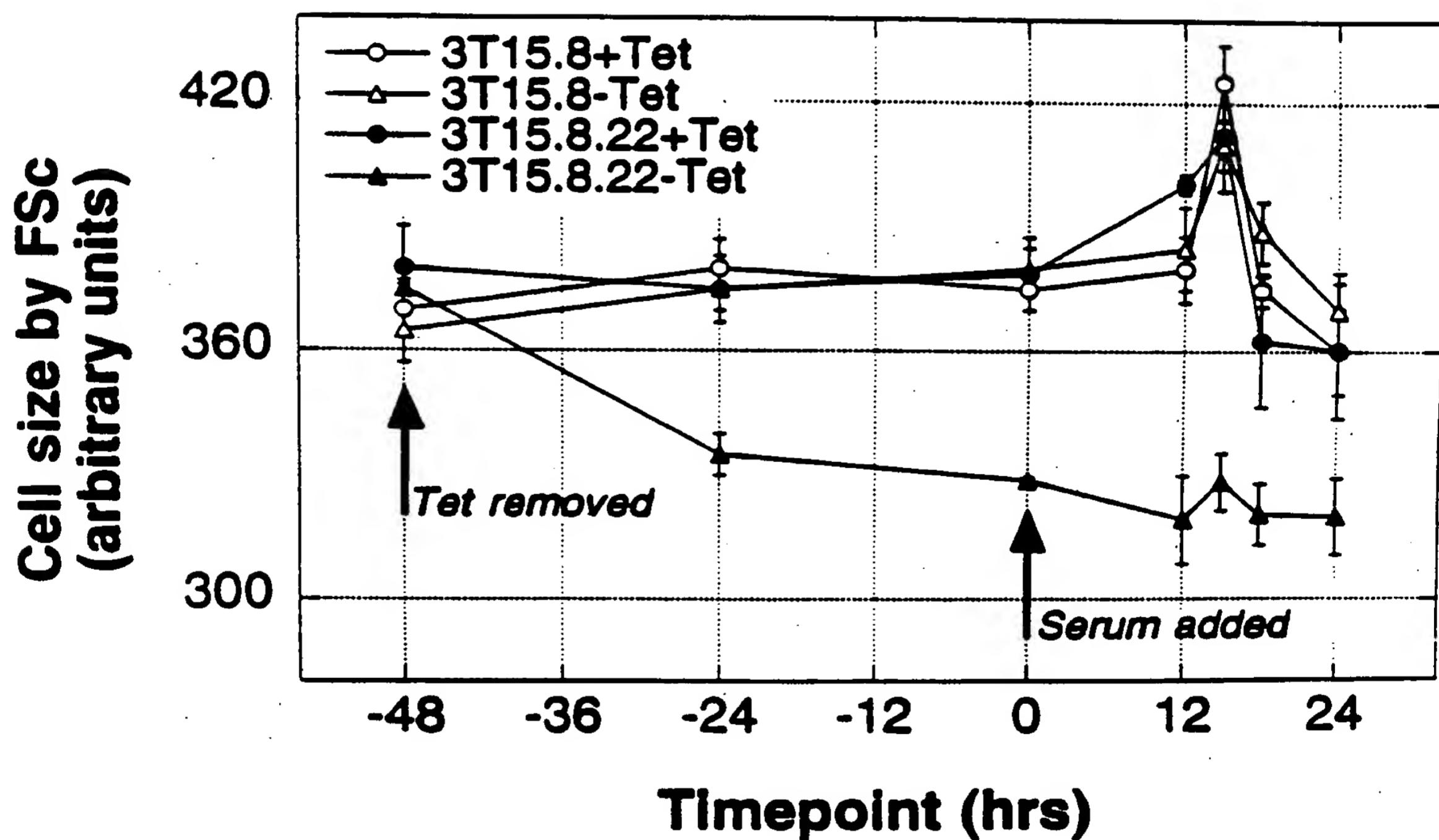
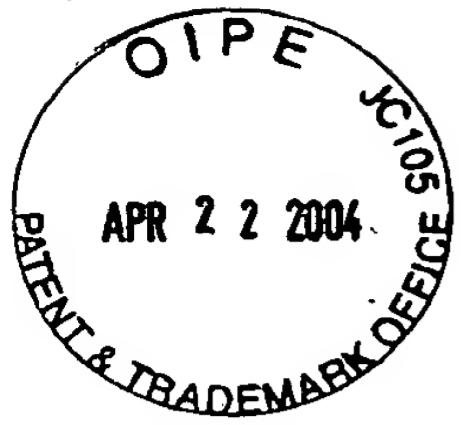


Fig. 9

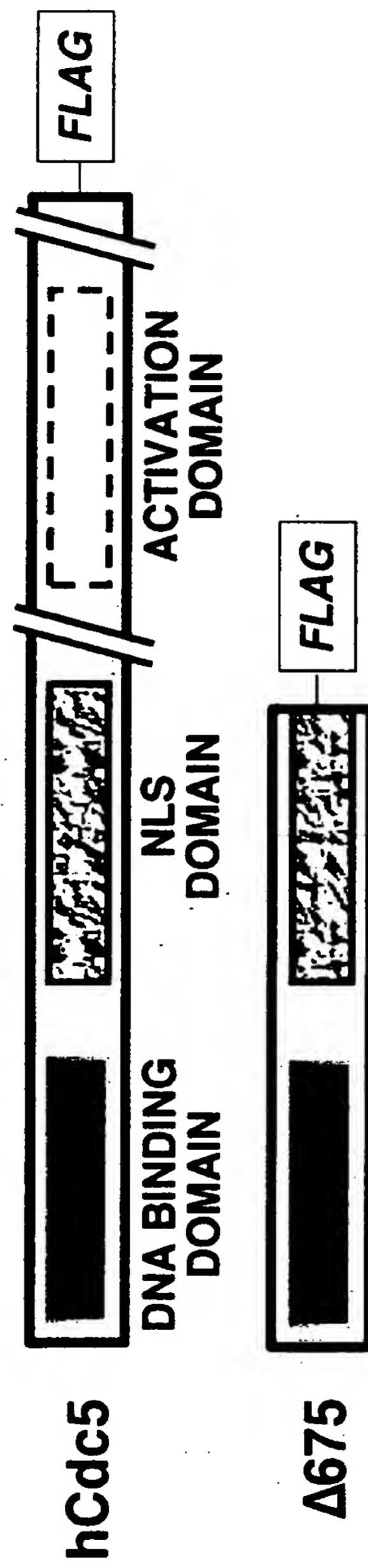


Fig. 10

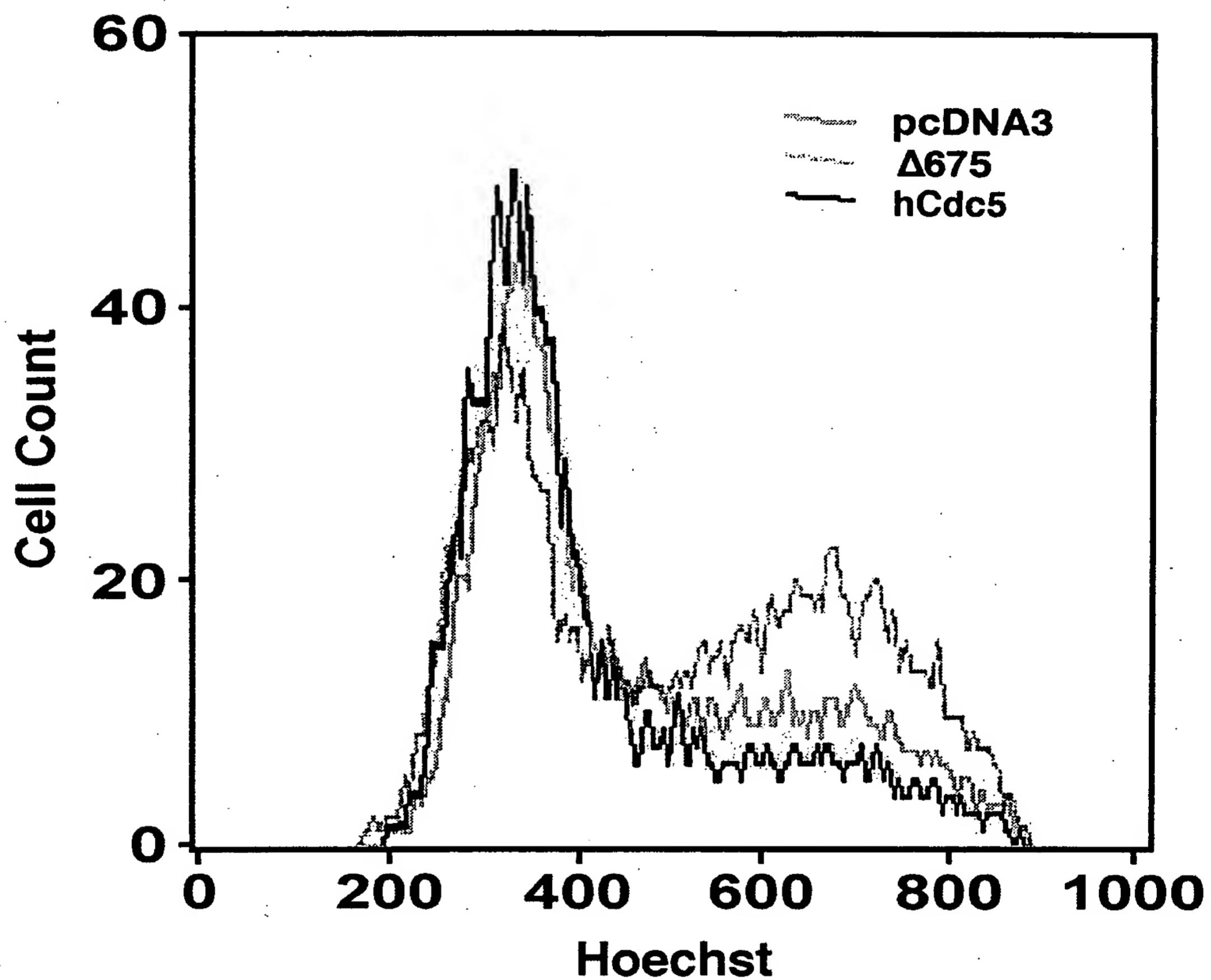


FIG. 11

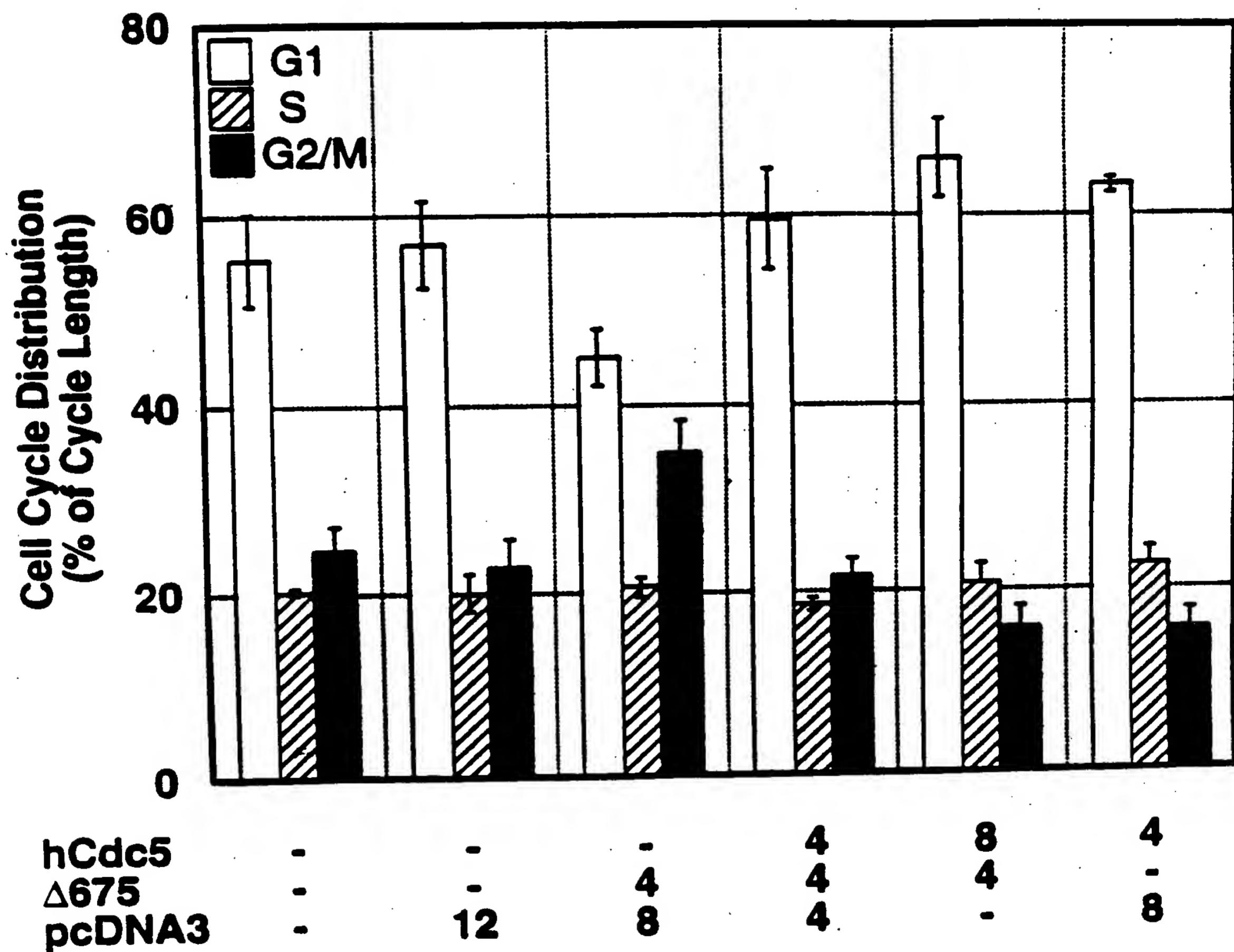


Fig. 12

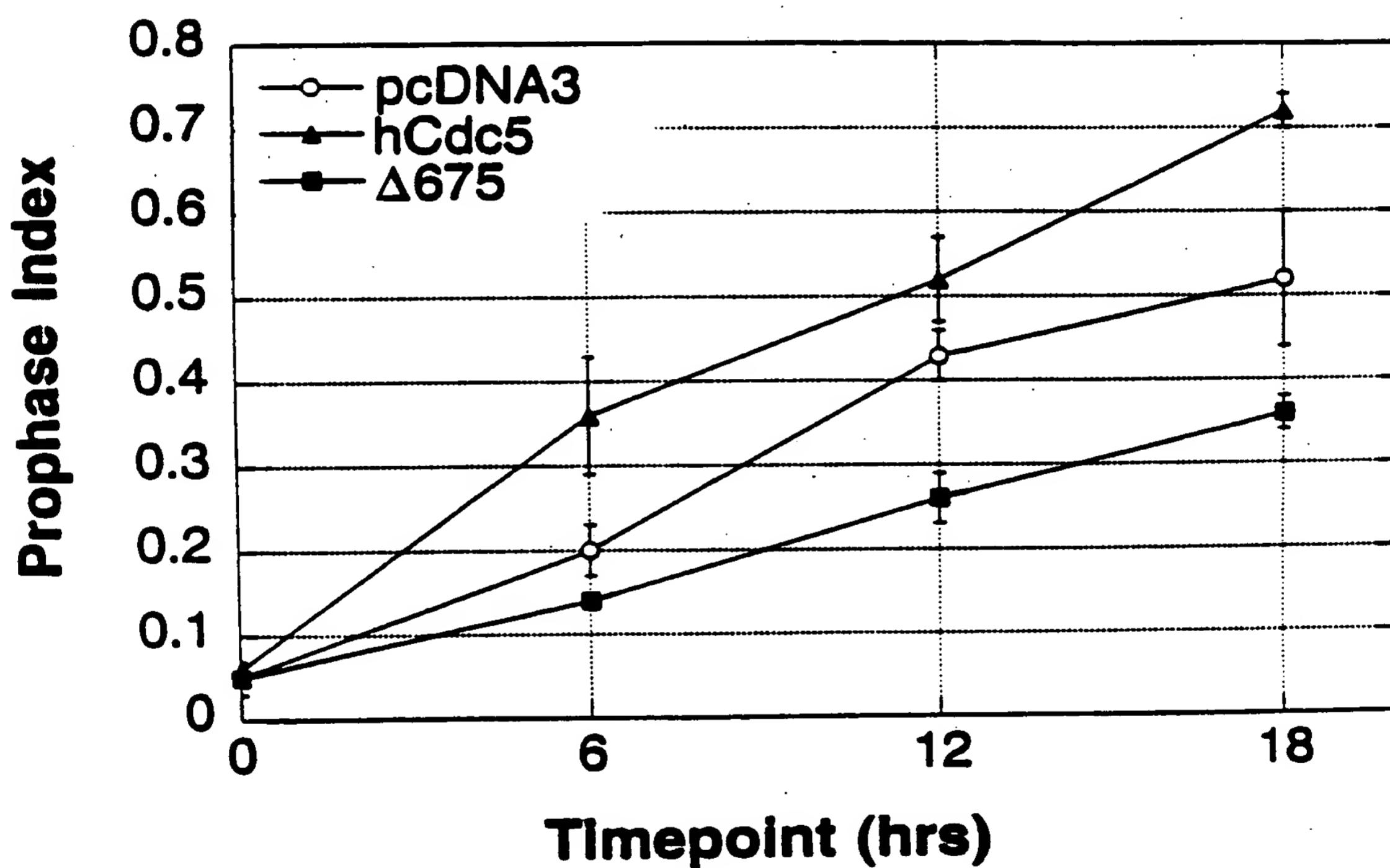


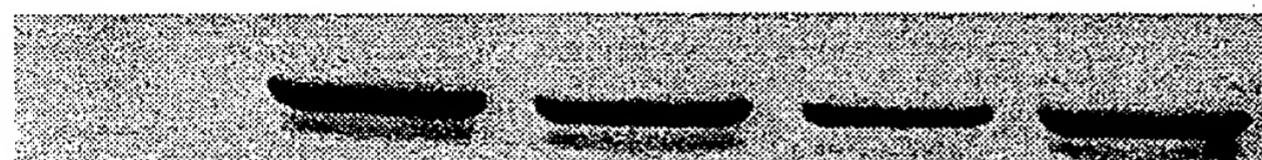
Fig. 13



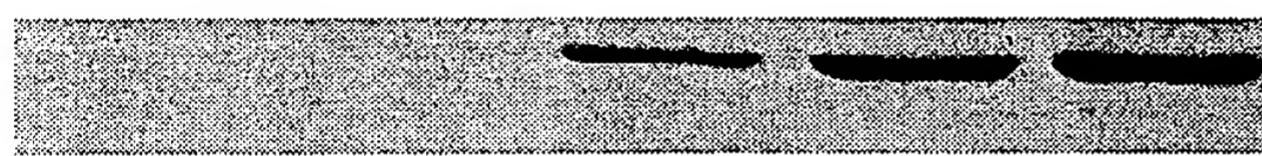
0 12 15 18 21 hrs



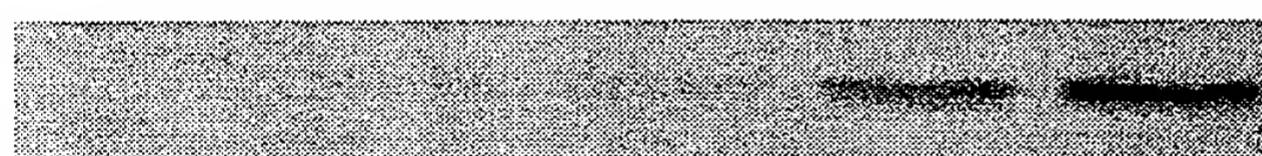
hCdc5



p50 CLNE



p60 CLNA



p62 CLNB1

FIG. 14A

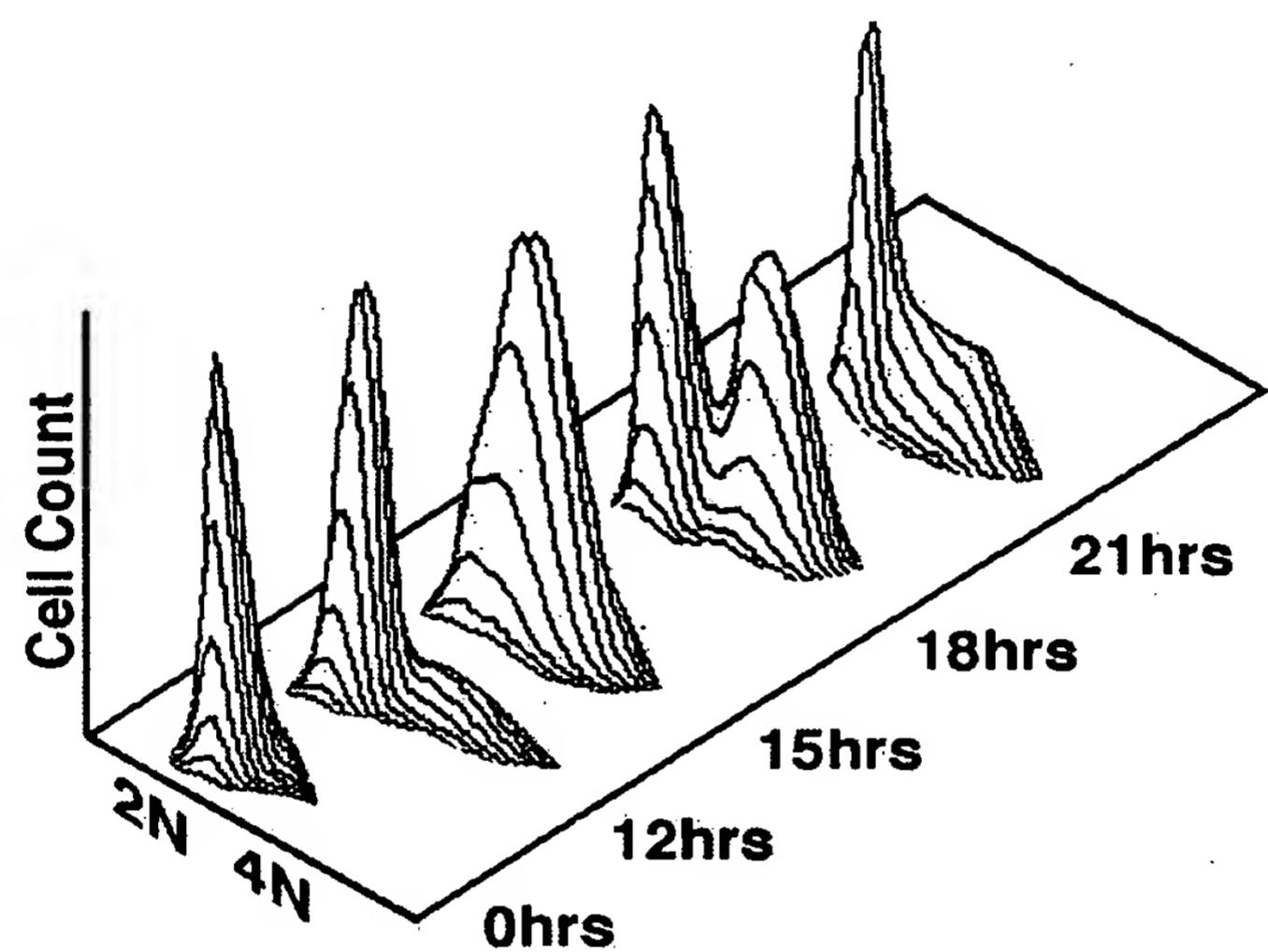


FIG. 14B



Consensus

G A T' T T A A C A T A A

(SEQ ID NO:13)

8.05 **G A T T T A A C A T A A**
8.04 **G A T T T A A C A T A A**
8.03 **G A T T T A A C A T A A**
8.02 **G A T T T A A C A T A A**
8.01 **G A T T T A A C A T A A**

6.05 **G G T G T A A C G G T G G** (SEQ ID NO:36)
6.04 **G T G T T A C C A C A T** (SEQ ID NO:37)
6.03 **C C A T A A A T T T A G** (SEQ ID NO:38)
6.02 **G A G A T A A A A G T C T** (SEQ ID NO:39)
6.01 **G T G T T A T T T G A A A** (SEQ ID NO:40)

3.05 **A C C C A C G T C T A T** (SEQ ID NO:41)
3.04 **G G T T A G G G A T A G G** (SEQ ID NO:42)
3.03 **G T T G A G T A G T A T** (SEQ ID NO:43)
3.02 **C T G T T A A T T T C C** (SEQ ID NO:44)
3.01 **G G T G T T A T T T G A T** (SEQ ID NO:45)

FIG 15